

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/762,097

DATE: 09/13/2001  
TIME: 17:29:08

Input Set : A:\1579-527 seq list.txt  
Output Set: N:\CRF3\09132001\I762097.raw

3 <110> APPLICANT: HERSHFIELD, MICHAEL S.  
4 KELLY, SUSAN J.  
6 <120> TITLE OF INVENTION: URATE OXIDASE  
8 <130> FILE REFERENCE: 1579-379  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/762,097  
C--> 11 <141> CURRENT FILING DATE: 2001-08-16  
13 <160> NUMBER OF SEQ ID NOS: 11  
15 <170> SOFTWARE: PatentIn Ver. 2.0  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 915  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Artificial Sequence ✓  
22 <220> FEATURE:  
23 <221> NAME/KEY: CDS  
24 <222> LOCATION: (1)..(915)  
26 <220> FEATURE:  
27 <223> OTHER INFORMATION: Description of Artificial Sequence:PBC CHIMERA ✓  
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32 1 5 10 15  
34 gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag 96  
35 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln  
36 20 25 30  
38 cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa 144  
39 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
40 35 40 45  
42 ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat 192  
43 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
44 50 55 60  
46 gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag 240  
47 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
48 65 70 75 80  
50 ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag 288  
51 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
52 85 90 95  
54 cat ttc ctt tct tcc aag cat gtc atc aga gct caa gtc tat gtg 336  
55 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
56 100 105 110  
58 gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc 384  
59 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
60 115 120 125  
62 cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa 432  
63 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
64 130 135 140  
66 cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta 480  
67 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu

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68	145	150	155	160	
70	aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac				528
71	Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp				
72	165	170	175		
74	cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa				576
75	Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln				
76	180	185	190		
78	gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag				624
79	Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu				
80	195	200	205		
82	gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg				672
83	Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly				
84	210	215	220		
86	ccc tat gac aaa ggc gag tac tca ccc tct gtg cag aag acc ctc tat				720
87	Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr				
88	225	230	235	240	
90	gat atc cag gtg ctc tcc ctg agc cga gtt cct gag ata gaa gat atg				768
91	Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met				
92	245	250	255		
94	gaa atc agc ctg cca aac att cac tac ttc aat ata gac atg tcc aaa				816
95	Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys				
96	260	265	270		
98	atg ggt ctg atc aac aag gaa gag gtc ttg ctg cca tta gac aat cca				864
99	Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro				
100	275	280	285		
102	tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg				912
103	Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu				
104	290	295	300		
106	tga				915

110 <210> SEQ ID NO: 2

111 <211> LENGTH: 304

112 <212> TYPE: PRT

113 <213> ORGANISM: Artificial Sequence

115 <220> FEATURE:

116 <223> OTHER INFORMATION: Description of Artificial Sequence: PBC CHIMERA

118 <400> SEQUENCE: 2

119	Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe			
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122	Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln			
123	20	25	30	
125	Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln			
126	35	40	45	
128	Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp			
129	50	55	60	
131	Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys			
132	65	70	75	80
134	Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu			
135	85	90	95	
137	His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val			

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138	100	105	110														
140	Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val	
141		115				120								125			
143	His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu	
144		130				135					140						
146	Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu	
147	145					150					155				160		
149	Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp	
150						165				170				175			
152	Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln	
153		180				185				190							
155	Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu	
156		195				200					205						
158	Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly	
159		210				215					220						
161	Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr	
162	225				230					235				240			
164	Asp	Ile	Gln	Val	Leu	Ser	Leu	Ser	Arg	Val	Pro	Glu	Ile	Glu	Asp	Met	
165					245				250				255				
167	Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys	
168		260				265					270						
170	Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro	
171		275				280					285						
173	Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu	
174		290				295					300						

177	<210> SEQ ID NO: 3	
178	<211> LENGTH: 915	
179	<212> TYPE: DNA	
180	<213> ORGANISM: Artificial Sequence	
182	<220> FEATURE:	
183	<221> NAME/KEY: CDS	
184	<222> LOCATION: (1)..(915)	
186	<220> FEATURE:	
187	<223> OTHER INFORMATION: Description of Artificial Sequence: pks chimera	
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192	1 5 10 15	
194	gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag	96
195	Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln	
196	20 25 30	
198	cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	144
199	Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
200	35 40 45	
202	ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
203	Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
204	50 55 60	
206	gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
207	Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	

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Input Set : A:\1579-527 seq list.txt  
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208	65	70	75	80	
210	ttc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag				288
211	Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu				
212	85	90	95		
214	cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg				336
215	His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val				
216	100	105	110		
218	gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc				384
219	Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val				
220	115	120	125		
222	cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa				432
223	His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu				
224	130	135	140		
226	cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta				480
227	Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu				
228	145	150	155	160	
230	aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac				528
231	Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp				
232	165	170	175		
234	cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa				576
235	Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln				
236	180	185	190		
238	gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag				624
239	Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu				
240	195	200	205		
242	gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg				672
243	Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly				
244	210	215	220		
246	ccc tat gac aaa ggc gag tac tcg ccc tct gtc cag aag aca ctc tat				720
247	Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr				
248	225	230	235	240	
250	gac atc cag gtg ctc acc ctg ggc cag gtt cct gag ata gaa gat atg				
251	Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met				
252	245	250	255		
254	gaa atc agc ctg cca aat att cac tac tta aac ata gac atg tcc aaa				816
255	Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys				
256	260	265	270		
258	atg gga ctg atc aac aag gaa gag gtc ttg cta cct tta gac aat cca				
259	Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro				
260	275	280	285		
262	tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg				912
263	Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu				
264	290	295	300		
266	tga				915
270	<210> SEQ ID NO: 4				
271	<211> LENGTH: 304				
272	<212> TYPE: PRT				
273	<213> ORGANISM: Artificial Sequence				
275	<220> FEATURE:				

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Input Set : A:\1579-527 seq list.txt  
Output Set: N:\CRF3\09132001\I762097.raw

276 <223> OTHER INFORMATION: Description of Artificial Sequence:pks chimera  
 278 <400> SEQUENCE: 4  
 279 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe  
 280 1 5 10 15  
 282 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln  
 283 20 25 30  
 285 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln  
 286 35 40 45  
 288 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp  
 289 50 55 60  
 291 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys  
 292 65 70 75 80  
 294 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu  
 295 85 90 95  
 297 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val  
 298 100 105 110  
 300 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val  
 301 115 120 125  
 303 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu  
 304 130 135 140  
 306 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu  
 307 145 150 155 160  
 309 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp  
 310 165 170 175  
 312 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln  
 313 180 185 190  
 315 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
 316 195 200 205  
 318 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly  
 319 210 215 220  
 321 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
 322 225 230 235 240  
 324 Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met  
 325 245 250 255  
 327 Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys  
 328 260 265 270  
 330 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
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